



## SEQUENCE LISTING

<110> University of Utah Research Foundation  
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<120> MinK-Related Genes, Formation of Potassium Channels and  
Association with Cardiac Arrhythmia

<130> 2323-150.a

<140> 09/550,163

<141> 2000-04-14

<150> US 60/129,404

<151> 1999-04-15

<160> 22

<170> PatentIn version 3.1/2.0

<210> 1

<211> 732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(442)

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Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu  
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gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157

Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln  
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aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205

Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu  
30 35 40

aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253

Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe  
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tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga 301

Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg  
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cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349

Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp  
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cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397

Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala  
95 100 105

acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc 442  
 Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro  
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 agaattttca tggagattat gtggttgcc aataaagata gatgacattt caatctcagt 622  
 gatttatgct tgcttggttg agcaatattt tgtgctgaag acctctttta ctttccgggc 682  
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 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile  
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 Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr  
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 <222> (35)..(403)

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 Thr Gln Thr Leu Glu Asp Ala Phe -Lys Lys Val Phe Ile Thr Tyr Met  
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gac agc tgg agg agg aac aca aca gcc gaa caa cag gcg ctc cag gcc 151  
 Asp Ser Trp Arg Arg Asn Thr Thr Ala Glu Gln Gln Ala Leu Gln Ala  
 25 30 35  
 aga gtg gat gcc gag aac ttc tac tac gtc atc ctg tac ctc atg gtg 199  
 Arg Val Asp Ala Glu Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val  
 40 45 50 55  
 atg atc ggc atg ttc gcc ttc atc gtg gtg gcc atc ctg gtg agc acg 247  
 Met Ile Gly Met Phe Ala Phe Ile Val Val Ala Ile Leu Val Ser Thr  
 60 65 70  
 gtg aag tcg aag cgg cgg gag cac tcc cag gac ccg tac cac cag tac 295  
 Val Lys Ser Lys Arg Arg Glu His Ser Gln Asp Pro Tyr His Gln Tyr  
 75 80 85  
 atc gtg gag gat tgg cag cag aag tat agg agt cag atc ttg cat ctg 343  
 Ile Val Glu Asp Trp Gln Gln Lys Tyr Arg Ser Gln Ile Leu His Leu  
 90 95 100  
 gaa gac tcc aag gcc acc atc cat gag aac ctg ggg gcg acg ggg ttc 391  
 Glu Asp Ser Lys Ala Thr Ile His Glu Asn Leu Gly Ala Thr Gly Phe  
 105 110 115  
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 Glu Gln Gln Ala Leu Gln Ala Arg Val Asp Ala Glu Asn Phe Tyr Tyr  
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 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ala Phe Ile Val  
 50 55 60  
 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser  
 65 70 75 80  
 Gln Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Gln Lys Tyr  
 85 90 95  
 Arg Ser Gln Ile Leu His Leu Glu Asp Ser Lys Ala Thr Ile His Glu  
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 Asn Leu Gly Ala Thr Gly Phe Thr Val Ser Pro  
 115 120

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<220>  
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 aaggaaactga ggggttgtgg gacatccacg aagagatcct caaagatgtc tcagagccag 180  
 cagagtctct gaactgtttg atcacattcc agctcttccc atacctcaat atctgttgct 240  
 atg gag act tcc aac ggg act gag acc tgg tac atg agc ctc cat gct 288  
 Met Glu Thr Ser Asn Gly Thr Glu Thr Trp Tyr Met Ser Leu His Ala  
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 gtg ctg aag gct ctg aac aca acc ctt cac agt cac ttg ctc tgc cgg 336  
 Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg  
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 cct ggg cca gga cca ggg cca gac aat caa act gag gat cgt cgg gct 384  
 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala  
                     35                    40                    45  
 agc ctt cct ggt cgt aat gac aac tcc tac atg tat att ctc ttt gtc 432  
 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val  
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 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr  
   65                    70                    75                    80  
 cgt tca cgc aaa gtg gac aaa cgt agt gac ccc tat cat gtg tac atc 528  
 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile  
                     85                    90                    95  
 aag aac cgt gtg tct atg atc tgatgtgagg aacctgaaga caatggaaga 579  
 Lys Asn Arg Val Ser Met Ile  
                     100  
 ttacaatgtc tgaggattgt cttctggtgc ctccggaact caactcaacc atatcaagcc 639  
 acagtgtatc tatgtaagat caacaggaaa ctggtaagag gattaggtca ttattaggac 699  
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 cgcattataa actcagagcc catgaacaca tatatataaa gtatggacaa ccagcaagta 819  
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           20                    25                    30  
 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala  
           35                    40                    45  
 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val  
       50                    55                    60  
 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr  
       65                    70                    75                    80  
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 <212> DNA  
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 <222> (604)..(1113)

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 ttaatagatg aatttttttc ctttattttc ttctgtctt tctttgttct aaggaaacat 180  
 tgttttgaat ttaaaatagt ttggttttgg aaacacaatg taaactttgt ttctgctcag 240  
 ttaaaatagc tttcccagtt ttaaagatac tatttactgt atgctcctgt cttacattga 300  
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 aaaaaaaaaa agtccttctt acttttccca gtgaaccttc cggggcttct ctcccgtgca 420  
 ctccaagccc tcatagctca ctcttgctcag ctggttggtt tatgctattt ctttcattga 480  
 cttttaagct tttttggtat tgcagttcca caaacctcgt gctccccccac ctccctggcc 540  
 caggacctgg gggagagtct aacctgcggc tttttcccag cccctgctgt ggaggcagcc 600  
 tca atg ctg aaa atg gag cct ctg aac agc acg cac ccc ggc acc gcc 648  
     Met Leu Lys Met Glu Pro Leu Asn Ser Thr His Pro Gly Thr Ala  
       1                    5                    10                    15

gcc tcc agc agc ccc ctg gag tcc cgt gcg gcc ggt ggc ggc agc ggc	696
Ala Ser Ser Ser Pro Leu Glu Ser Arg Ala Ala Gly Gly Gly Ser Gly	
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aat ggc aac gag tac ttc tac att ctg gtt gtc atg tcc ttc tac ggc	744
Asn Gly Asn Glu Tyr Phe Tyr Ile Leu Val Val Met Ser Phe Tyr Gly	
35 40 45	
att ttc ttg atc gga atc atg ctg ggc tac atg aaa tcc aag agg cgg	792
Ile Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg	
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gag aag aag tcc agc ctc ctg ctg ctg tac aaa gac gag gag cgg ctc	840
Glu Lys Lys Ser Ser Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu	
65 70 75	
tgg ggg gag gcc atg aag ccg ctg ccc gtg gtg tcg ggc ctg agg tcg	888
Trp Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser	
80 85 90 95	
gtg cag gtg ccc ctg atg ctg aac atg ctg cag gag agc gtg gcg ccc	936
Val Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro	
100 105 110	
gcg ctg tcc tgc acc ctc tgt tcc atg gaa ggg gac agc gtg agc tcc	984
Ala Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser	
115 120 125	
gag tcc tcc tcc ccg gac gtg cac ctc acc att cag gag gag ggg gca	1032
Glu Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala	
130 135 140	
gac gat gag ctg gag gag acc tcg gag acg ccc ctc aac gag agc agc	1080
Asp Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Glu Ser Ser	
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Glu Gly Ser Ser Glu Asn Ile His Gln Asn Ser	
160 165 170	
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taagagatga tcttctatct tgaccttttg tctaacttat gaccttgaac tctgacctgt	1793
gaccatgcag catcacatga tggcatgacg ttctttggat cagaagagct tccccagaat	1853

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 <213> Homo sapiens

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 Gly Asn Glu Tyr Phe Tyr Ile Leu Val Val Met Ser Phe Tyr Gly Ile  
             35                    40                    45  
 Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu  
             50                    55                    60  
 Lys Lys Ser Ser Leu Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp  
             65                    70                    75                    80  
 Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser Val  
                     85                    90                    95  
 Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala  
             100                    105                    110  
 Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu  
             115                    120                    125  
 Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala Asp  
             130                    135                    140  
 Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Glu Ser Ser Glu  
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 <213> Mus musculus

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 Thr Tyr Pro Ser Ala Ala Ala Ser Ser Ser Pro Leu Glu Ser His Val  
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Pro Ser Asn Ser Ser Gly Asn Gly Asn Glu Tyr Phe Tyr Ile Leu Val	
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Val Met Ser Phe Tyr Gly Val Phe Leu Ile Gly Ile Met Leu Gly Tyr	
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Met Lys Ser Lys Arg Arg Glu Lys Lys Ser Ser Leu Leu Leu Leu Tyr	
60 65 70	
aaa gac gag gag agg ctg tgg ggg gag gct atg aag ccg cta cct atg	352
Lys Asp Glu Glu Arg Leu Trp Gly Glu Ala Met Lys Pro Leu Pro Met	
75 80 85	
atg tcc ggc ttg agg tca ggg cag gtg ccc atg atg ctg aat atg ctg	400
Met Ser Gly Leu Arg Ser Gly Gln Val Pro Met Met Leu Asn Met Leu	
90 95 100 105	
cag gag agt gtg gcg ccg gca ctg tcc tgc act ctt tgc tcg atg gaa	448
Gln Glu Ser Val Ala Pro Ala Leu Ser Cys Thr Leu Cys Ser Met Glu	
110 115 120	
ggg gac agt gtg agc tcc gag tcc tcc tct cct gat gtg cac ctt ccc	496
Gly Asp Ser Val Ser Ser Glu Ser Ser Ser Pro Asp Val His Leu Pro	
125 130 135	
atc cag gag gag ggg gct gat gac gag ctg gag gag acc tcc gag acg	544
Ile Gln Glu Glu Gly Ala Asp Asp Glu Leu Glu Glu Thr Ser Glu Thr	
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cct ctc aac gac agc agt gaa ggc tct tcc gag aac atc cac cag aat	592
Pro Leu Asn Asp Ser Ser Glu Gly Ser Ser Glu Asn Ile His Gln Asn	
155 160 165	
tcc tagcaccac caggtgctag gaggtagctc cgtaagctac acttgacaga	645
Ser	
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actgagggca agctccaaaa tggggcaggg agagacaagg ctcagctgca gtccttgagg	765
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 cactataagg agctgttttt ttcaatcagt ttgacacag agatagaaag gtaatttatg 2145  
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 gctgagttgt agacaattgt ctggtgtatt taatggtttg taattttcac gatatttttt 2445  
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 35 40 45  
 Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu  
 50 55 60  
 Lys Lys Ser Ser Leu Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp  
 65 70 75 80  
 Gly Glu Ala Met Lys Pro Leu Pro Met Met Ser Gly Leu Arg Ser Gly  
 85 90 95  
 Gln Val Pro Met Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala

100	105	110
Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu		
115	120	125
Ser Ser Ser Pro Asp Val His Leu Pro Ile Gln Glu Glu Gly Ala Asp		
130	135	140
Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Asp Ser Ser Glu		
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Gly Ser Ser Glu Asn Ile His Gln Asn Ser		
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<220>  
 <223> Description of Artificial Sequence:PCR primer for  
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<210> 14  
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<210> 15  
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 mutation screening

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 mutation screening

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 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PCR primer for  
 mutation screening

<400> 18  
 tgtctggacg tcagatgtta g

21

<210> 19  
 <211> 09  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HA residues for  
 epitope mapping

<400> 19  
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
 1 5

<210> 20  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:cmv residues  
 for epitope-mapping

<400> 20  
 Ile Ser Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 1 5 10

<210> 21  
 <211> 130  
 <212> PRT  
 <213> rattus norvegicus

<400> 21  
 Met Ala Leu Ser Asn Ser Thr Thr Val Leu Pro Phe Leu Ala Ser Leu

1	5	10	15
Trp Gln Glu Thr Asp Glu Pro Gly Gly Asn Met Ser Ala Asp Leu Ala	20	25	30
Arg Arg Ser Gln Leu Arg Asp Asp Ser Lys Leu Glu Ala Leu Tyr Ile	35	40	45
Leu Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu	50	55	60
Ser Tyr Ile Arg Ser Lys Lys Leu Glu His Ser His Asp Pro Phe Asn	65	70	75
Val Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Gly Lys Ala Leu Phe	85	90	95
Gln Ala Arg Val Leu Glu Ser Phe Arg Ala Cys Tyr Val Ile Glu Asn	100	105	110
Gln Ala Ala Val Glu Gln Pro Ala Thr His Leu Pro Glu Leu Lys Pro	115	120	125
Leu Ser	130		

<210> 22  
 <211> 129  
 <212> PRT  
 <213> homo sapiens

<400> 22  
 Met Ile Leu Ser Asn Thr Thr Ala Val Thr Pro Phe Leu Thr Lys Leu  
 1 5 10 15  
 Trp Gln Glu Thr Val Gln Gln Gly Gly Asn Met Ser Gly Leu Ala Arg  
 20 25 30  
 Arg Ser Pro Arg Ser Gly Asp Gly Lys Leu Glu Ala Leu Tyr Val Leu  
 35 40 45  
 Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu Ser  
 50 55 60  
 Tyr Ile Arg Ser Lys Lys Leu Glu His Ser Asn Asp Pro Phe Asn Val  
 65 70 75 80  
 Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Asp Lys Ala Tyr Val Gln  
 85 90 95  
 Ala Arg Val Leu Glu Ser Tyr Arg Ser Cys Tyr Val Val Glu Asn His  
 100 105 110  
 Leu Ala Ile Glu Gln Pro Asn Thr His Leu Pro Glu Thr Lys Pro Ser  
 115 120 125  
 Pro